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APAND et al  
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<110> ARAND, MICHAEL  
ARCHELAS, ALAIN ROBERT  
BARATI, JACQUES  
FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030

<141> 2001-11-02

<150> PCT/FR00/01217

<151> 2000-05-05

<150> FR 99/05711

<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1197

<212> DNA

<213> Aspergillus niger

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<221> CDS

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aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96  
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys  
20 25 30

acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144  
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
35 40 45

caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192  
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
50 55 60

cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240  
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
65 70 75 80

ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288  
Leu Asn Ser Phe Pro Gln Phe Thr Glu Ile Glu Gly Leu Thr Ile  
85 90 95

cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336  
 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384  
 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg 432  
 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg 480  
 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
 145 150 155 160

gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg 528  
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 165 170 175

atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat 576  
 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190

att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc 624  
 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205

aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc 672  
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220

ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga 720  
 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240

atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt 768  
 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
 245 250 255

act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca 816  
 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala  
 260 265 270

tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc 864  
 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
 275 280 285

ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg 912  
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 290 295 300

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 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
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gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
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cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg 1056  
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 340 345 350

cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
 355 360 365

cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152  
 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
 370 375 380

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 35 40 45

Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
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Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu  
 165 170 175  
 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190  
 Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205  
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220  
 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240  
 Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
 245 250 255  
 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala  
 260 265 270  
 Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
 275 280 285  
 Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr  
 290 295 300  
 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
 305 310 315 320  
 Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
 325 330 335  
 His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val  
 340 345 350  
 Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
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<223> Description of Artificial Sequence: Primer

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<212> DNA  
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<223> Description of Artificial Sequence: Primer

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44

## SEQUENCE LISTING

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5 <120> PROTEINS OF FUNGAL ORIGIN AND DERIVATIVES,  
 PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN  
 PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY  
 PURE MOLECULES

10 &lt;130&gt; EPOXSL

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15 &lt;160&gt; 2

&lt;170&gt; PatentIn Ver. 2.1

20 <210> 1  
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Nucleotide sequence SEQ ID NO : 1

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35 aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96  
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 20 25 30

40 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144  
 Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

45 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192  
 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

55 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240  
 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

50 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288  
 Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

55 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336  
 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

60 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384  
 Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

5	cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu 130 135 140	432
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15	gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu 165 170 175	528
20	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp 180 185 190	576
25	att ggt agc ttt gtt gga cga ctg ttg ggc gtc ggt ttc gac gcc tgc Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys 195 200 205	624
30	aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly 210 215 220	672
35	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg 225 230 235 240	720
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50	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro 275 280 285	864
55	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr 290 295 300	912
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65	gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile 325 330 335	1008
70	cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val 340 345 350	1056
75	cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp 355 360 365	1104

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 His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
 .370 375 380

5 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197  
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<213> Aspergillus niger

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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu  
 35 40 45

25 Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met  
 50 55 60

30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg  
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile  
 85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala  
 100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu  
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu  
 130 135 140

45 Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu  
 145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu  
 165 170 175

50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp  
 180 185 190

Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys  
 195 200 205

55 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly  
 210 215 220

60 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg  
 225 230 235 240

Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser  
245 250 255

5 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala  
260 265 270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro  
10 275 280 285

Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr  
290 295 300

15 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr  
305 310 315 320

Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile  
325 330 335

20 His Lys Pro Phe Gly Phe Ser Phe Pro Lys Asp Leu Cys Pro Val  
340 345 350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp  
25 355 360 365

His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu  
370 375 380

30 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys  
385 390 395